

SEQUENCE LISTING

DT09 Rec'd PCT/PTO '26 AUG 2005

<110> JACQUET, Alain

<120> HYPOALLERGENIC DER P1 AND DER P3 PROTEINS FROM DERMATOGRAPHOIDES
PTERONYSSINUS

<130> VB60107

<140> PCT/EP2004/001850
24-02-2004<150> GB 0304424.5
26-02-2003

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 909

<212> DNA

<213> Dermatophagoides pteronyssinus

<220>

<221> CDS

<222> (1)...(906)

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aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc	96
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe	
20 25 30	
ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac	144
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His	
35 40 45	
ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc	192
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser	
50 55 60	
gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag	240

Ala	Glu	Ala	Phe	Glu	His	Leu	Lys	Thr	Gln	Phe	Asp	Leu	Asn	Ala	Glu	
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acc	aac	gcc	tgc	agt	atc	aac	ggc	aat	gcc	ccc	gct	gag	att	gat	ctg	288
Thr	Asn	Ala	Cys	Ser	Ile	Asn	Gly	Asn	Ala	Pro	Ala	Glu	Ile	Asp	Leu	
				85					90					95		
cgc	cag	atg	agg	acc	gtg	act	ccc	atc	cgc	atg	caa	ggc	ggc	tgc	ggg	336
Arg	Gln	Met	Arg	Thr	Val	Thr	Pro	Ile	Arg	Met	Gln	Gly	Gly	Cys	Gly	
			100					105					110			
tct	tgt	tgg	gcc	ttt	tca	ggc	gtg	gcc	gcg	aca	gag	tcg	gca	tac	ctc	384
Ser	Cys	Trp	Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr	Glu	Ser	Ala	Tyr	Leu	
		115					120					125				
gcg	tat	cgg	aat	cag	agc	ctg	gac	ctc	gct	gag	cag	gag	ctc	gtt	gac	432
Ala	Tyr	Arg	Asn	Gln	Ser	Leu	Asp	Leu	Ala	Glu	Gln	Glu	Leu	Val	Asp	
	130					135				140						
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Cys	Ala	Ser	Gln	His	Gly	Cys	His	Gly	Asp	Thr	Ile	Pro	Arg	Gly	Ile	
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gaa	tac	atc	cag	cat	aat	ggc	gtc	gtg	cag	gaa	agc	tat	tac	cga	tac	528
Glu	Tyr	Ile	Gln	His	Asn	Gly	Val	Val	Gln	Glu	Ser	Tyr	Tyr	Arg	Tyr	
				165					170					175		
gta	gct	agg	gag	cag	tcc	tgc	cgc	cgt	cct	aac	gca	cag	cgc	ttc	ggc	576
Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg	Phe	Gly	
			180					185					190			
att	tcc	aat	tat	tgc	cag	atc	tac	ccc	cct	aat	gcc	aac	aag	atc	agg	624
Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Ala	Asn	Lys	Ile	Arg	
		195					200					205				
gag	gcc	ctg	gcg	cag	acg	cac	agc	gcc	atc	gct	gtc	atc	atc	gga	atc	672
Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile	
	210					215					220					
aag	gat	ctg	gac	gca	ttc	cgg	cac	tat	gac	ggg	cgc	aca	atc	atc	cag	720
Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln	
225					230					235					240	
cgc	gac	aac	gga	tat	cag	cca	aac	tac	cac	gcg	gtc	aac	atc	gtg	ggt	768
Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala	Val	Asn	Ile	Val	Gly	
				245					250					255		

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
275 280 285

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taa 909

<210> 2

<211> 302

<212> PRT

<213> Dermatophagoides pteronyssinus

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20 25 30
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
35 40 45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
50 55 60
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65 70 75 80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
85 90 95
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
100 105 110
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
115 120 125
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
130 135 140
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile
145 150 155 160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
165 170 175
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
180 185 190
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg

195	200	205
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile		
210	215	220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln		
225	230	235
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly		
245	250	255
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp		
260	265	270
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile		
275	280	285
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu		
290	295	300

<210> 3

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> C4R mutant of ProDer p 1

<400> 3

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn		
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Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His		
35	40	45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser		
50	55	60
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu		
65	70	75
Thr Asn Ala Arg Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu		
85	90	95
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly		
100	105	110
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu		
115	120	125
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp		
130	135	140
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile		
145	150	155
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr		
165	170	175

Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg	Phe	Gly
			180					185					190		
Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Val	Asn	Lys	Ile	Arg
		195					200					205			
Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile
	210					215					220				
Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln
225					230					235					240
Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala	Val	Asn	Ile	Val	Gly
			245					250					255		
Tyr	Ser	Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	Val	Arg	Asn	Ser	Trp
		260						265					270		
Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala	Asn	Ile
	275						280					285			
Asp	Leu	Met	Met	Ile	Glu	Glu	Tyr	Pro	Tyr	Val	Val	Ile	Leu		
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<210> 4

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<221> CDS

<222> (1)...(906)

<223> C4R mutant of ProDer p 1

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Arg	Pro	Ser	Ser	Ile	Lys	Thr	Phe	Glu	Glu	Tyr	Lys	Lys	Ala	Phe	Asn	
1			5					10					15			

aag	agc	tat	gcc	acc	ttc	gag	gac	gag	gag	gcc	gcg	cgc	aag	aac	ttc	96
Lys	Ser	Tyr	Ala	Thr	Phe	Glu	Asp	Glu	Glu	Ala	Ala	Arg	Lys	Asn	Phe	
			20					25					30			

ctg	gaa	agc	gtg	aaa	tac	gtg	cag	agc	aac	ggc	ggg	gct	ata	aat	cac	144
Leu	Glu	Ser	Val	Lys	Tyr	Val	Gln	Ser	Asn	Gly	Gly	Ala	Ile	Asn	His	
			35					40					45			

ctg	tcc	gac	ctg	tct	tta	gac	gag	ttc	aag	aac	cgg	ttc	ctg	atg	agc	192
Leu	Ser	Asp	Leu	Ser	Leu	Asp	Glu	Phe	Lys	Asn	Arg	Phe	Leu	Met	Ser	
			50				55					60				

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag	240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu	
65 70 75 80	
acc aac gcc cgt agt atc aac ggc aat gcc ccc gct gag att gat ctg	288
Thr Asn Ala Arg Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu	
85 90 95	
cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg	336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly	
100 105 110	
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc	384
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu	
115 120 125	
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac	432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp	
130 135 140	
tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc	480
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile	
145 150 155 160	
gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac	528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr	
165 170 175	
gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc	576
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly	
180 185 190	
att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg	624
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg	
195 200 205	
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc	672
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile	
210 215 220	
aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag	720
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln	
225 230 235 240	
cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt	768
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly	

245	250	255	
tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg			816
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp			
260	265	270	
gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc			864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile			
275	280	285	
gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg			906
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu			
290	295	300	
taa			909
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Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe			
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Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His			
35	40	45	
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser			
50	55	60	
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu			
65	70	75	80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu			
85	90	95	
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Arg Gly			
100	105	110	
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
115	120	125	
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			
130	135	140	
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile			
145	150	155	160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr			

				165						170					175				
Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg	Phe	Gly				
			180						185					190					
Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Val	Asn	Lys	Ile	Arg				
		195					200					205							
Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile				
	210					215					220								
Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln				
225				230					235					240					
Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala	Val	Asn	Ile	Val	Gly				
		245					250					255							
Tyr	Ser	Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	Val	Arg	Asn	Ser	Trp				
		260					265					270							
Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala	Asn	Ile				
	275					280					285								
Asp	Leu	Met	Met	Ile	Glu	Glu	Tyr	Pro	Tyr	Val	Val	Ile	Leu						
	290					295					300								

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<211> 909

<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (1)...(906)

<223> C31R mutant of ProDer p 1

<400> 6

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Arg	Pro	Ser	Ser	Ile	Lys	Thr	Phe	Glu	Glu	Tyr	Lys	Lys	Ala	Phe	Asn	
1			5					10					15			

aag	agc	tat	gcc	acc	ttc	gag	gac	gag	gag	gcc	gcg	cgc	aag	aac	ttc	96
Lys	Ser	Tyr	Ala	Thr	Phe	Glu	Asp	Glu	Glu	Ala	Ala	Arg	Lys	Asn	Phe	
		20				25						30				

ctg	gaa	agc	gtg	aaa	tac	gtg	cag	agc	aac	ggc	ggg	gct	ata	aat	cac	144
Leu	Glu	Ser	Val	Lys	Tyr	Val	Gln	Ser	Asn	Gly	Gly	Ala	Ile	Asn	His	
	35					40						45				

ctg	tcc	gac	ctg	tct	tta	gac	gag	ttc	aag	aac	cgg	ttc	ctg	atg	agc	192
Leu	Ser	Asp	Leu	Ser	Leu	Asp	Glu	Phe	Lys	Asn	Arg	Phe	Leu	Met	Ser	
	50					55					60					

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag	240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu	
65 70 75 80	
acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg	288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu	
85 90 95	
cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc cgt ggg	336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Arg Gly	
100 105 110	
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc	384
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu	
115 120 125	
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac	432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp	
130 135 140	
tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc	480
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile	
145 150 155 160	
gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac	528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr	
165 170 175	
gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc	576
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly	
180 185 190	
att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg	624
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg	
195 200 205	
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc	672
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile	
210 215 220	
aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag	720
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln	
225 230 235 240	
cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt	768

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly	
245 250 255	
tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg	816
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp	
260 265 270	
gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc	864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile	
275 280 285	
gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg	906
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu	
290 295 300	
taa	909
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Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His	
35 40 45	
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser	
50 55 60	
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu	
65 70 75 80	
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu	
85 90 95	
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly	
100 105 110	
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu	
115 120 125	
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp	
130 135 140	
Arg Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile	
145 150 155 160	

50	55	60	
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Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu			
65	70	75	80
acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg			288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu			
	85	90	95
cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg			336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly			
	100	105	110
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc			384
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
	115	120	125
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac			432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			
	130	135	140
cgt gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc			480
Arg Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile			
	145	150	155
			160
gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac			528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr			
	165	170	175
gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc			576
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly			
	180	185	190
att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg			624
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg			
	195	200	205
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc			672
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile			
	210	215	220
aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag			720
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln			
	225	230	235
			240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
 245 250 255

 tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
 260 265 270

 gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
 275 280 285

 gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
 290 295 300

 taa 909

<210> 9

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> C71R mutant of ProDer p 1

<400> 9

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
 1 5 10 15
 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
 20 25 30
 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
 35 40 45
 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
 50 55 60
 Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
 65 70 75 80
 Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
 85 90 95
 Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
 100 105 110
 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
 115 120 125
 Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
 130 135 140
 Cys Ala Ser Gln His Gly Arg His Gly Asp Thr Ile Pro Arg Gly Ile

145		150		155		160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr						
	165		170		175	
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly						
	180		185		190	
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg						
	195		200		205	
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile						
	210		215		220	
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln						
225		230		235		240
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly						
	245		250		255	
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp						
	260		265		270	
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile						
	275		280		285	
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu						
	290		295		300	

<210> 10
 <211> 909
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(906)

<223> C71R mutant of ProDer p 1

<400> 10	
cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac	48
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn	
1 5 10 15	
aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc	96
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe	
20 25 30	
ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac	144
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His	
35 40 45	
ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc	192

Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser	
50 55 60	
gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag	240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu	
65 70 75 80	
acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg	288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu	
85 90 95	
cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg	336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly	
100 105 110	
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc	384
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu	
115 120 125	
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac	432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp	
130 135 140	
tgc gcc tcc caa cac gga cgt cat ggg gat acg att ccc aga ggt atc	480
Cys Ala Ser Gln His Gly Arg His Gly Asp Thr Ile Pro Arg Gly Ile	
145 150 155 160	
gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac	528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr	
165 170 175	
gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc	576
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly	
180 185 190	
att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg	624
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg	
195 200 205	
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc	672
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile	
210 215 220	
aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag	720
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln	
225 230 235 240	

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
 245 250 255

 tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
 260 265 270

 gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
 275 280 285

 gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
 290 295 300

 taa 909

<210> 11
 <211> 302
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> C103R mutant of ProDer p 1

<400> 11
 Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
 1 5 10 15
 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
 20 25 30
 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
 35 40 45
 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
 50 55 60
 Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
 65 70 75 80
 Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
 85 90 95
 Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
 100 105 110
 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
 115 120 125
 Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
 130 135 140

Cys	Ala	Ser	Gln	His	Gly	Cys	His	Gly	Asp	Thr	Ile	Pro	Arg	Gly	Ile
145					150					155					160
Glu	Tyr	Ile	Gln	His	Asn	Gly	Val	Val	Gln	Glu	Ser	Tyr	Tyr	Arg	Tyr
			165						170						175
Val	Ala	Arg	Glu	Gln	Ser	Arg	Arg	Arg	Pro	Asn	Ala	Gln	Arg	Phe	Gly
			180						185					190	
Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Val	Asn	Lys	Ile	Arg
		195						200					205		
Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile
	210					215					220				
Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln
225					230					235					240
Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala	Val	Asn	Ile	Val	Gly
			245						250						255
Tyr	Ser	Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	Val	Arg	Asn	Ser	Trp
			260						265					270	
Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala	Asn	Ile
		275					280					285			
Asp	Leu	Met	Met	Ile	Glu	Glu	Tyr	Pro	Tyr	Val	Val	Ile	Leu		
	290					295					300				

<210> 12

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(906)

<223> C103R mutant of ProDer p 1

<400> 12

cgg ccg agc tcc att aag acc ttc gag gaa tac aag aaa gcc ttc aac 48

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn

1 5 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96

Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144

Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His

35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc	192
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser	
50 55 60	
gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag	240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu	
65 70 75 80	
acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg	288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu	
85 90 95	
cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg	336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly	
100 105 110	
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc	384
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu	
115 120 125	
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac	432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp	
130 135 140	
tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc	480
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile	
145 150 155 160	
gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac	528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr	
165 170 175	
gta gct agg gag cag tcc cgt cgc cgt cct aac gca cag cgc ttc ggc	576
Val Ala Arg Glu Gln Ser Arg Arg Arg Pro Asn Ala Gln Arg Phe Gly	
180 185 190	
att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg	624
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg	
195 200 205	
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc	672
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile	
210 215 220	
aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag	720
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln	

225	230	235	240	
cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt				768
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly				
245	250	255		
tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg				816
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp				
260	265	270		
gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc				864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile				
275	280	285		
gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg				906
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu				
290	295	300		
taa				909

<210> 13
 <211> 302
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> C117R mutant of ProDer p 1

<400> 13

Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn			
1	5	10	15
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe			
20	25	30	
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His			
35	40	45	
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser			
50	55	60	
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu			
65	70	75	80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu			
85	90	95	
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly			
100	105	110	
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
115	120	125	
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			

130		135		140
Cys Ala Ser Gln His Gly	Cys His Gly Asp Thr	Ile Pro Arg Gly Ile		
145	150	155	160	
Glu Tyr Ile Gln His Asn Gly	Val Val Gln Glu Ser Tyr Tyr	Arg Tyr		
	165	170	175	
Val Ala Arg Glu Gln Ser Cys Arg	Arg Pro Asn Ala Gln Arg Phe Gly			
	180	185	190	
Ile Ser Asn Tyr Arg Gln Ile Tyr	Pro Pro Asn Val Asn Lys Ile Arg			
	195	200	205	
Glu Ala Leu Ala Gln Thr His Ser	Ala Ile Ala Val Ile Ile Gly Ile			
	210	215	220	
Lys Asp Leu Asp Ala Phe Arg His Tyr	Asp Gly Arg Thr Ile Ile Gln			
	225	230	235	240
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr	His Ala Val Asn Ile Val Gly			
	245	250	255	
Tyr Ser Asn Ala Gln Gly Val Asp Tyr	Trp Ile Val Arg Asn Ser Trp			
	260	265	270	
Asp Thr Asn Trp Gly Asp Asn Gly Tyr	Gly Tyr Phe Ala Ala Asn Ile			
	275	280	285	
Asp Leu Met Met Ile Glu Glu Tyr Pro	Tyr Val Val Ile Leu			
	290	295	300	

<210> 14

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(906)

<223> C117R mutant of ProDer p 1

<400> 14

cg	g	ccg	agc	tcc	att	aag	acc	ttc	gag	gaa	tac	aag	aaa	gcc	ttc	aac	48
Arg	Pro	Ser	Ser	Ile	Lys	Thr	Phe	Glu	Glu	Tyr	Lys	Lys	Ala	Phe	Asn		
1				5						10					15		

aag	agc	tat	gcc	acc	ttc	gag	gac	gag	gag	gcc	gcg	cgc	aag	aac	ttc	96
Lys	Ser	Tyr	Ala	Thr	Phe	Glu	Asp	Glu	Glu	Ala	Ala	Arg	Lys	Asn	Phe	
			20					25					30			

ctg	gaa	agc	gtg	aaa	tac	gtg	cag	agc	aac	ggc	ggg	gct	ata	aat	cac	144
Leu	Glu	Ser	Val	Lys	Tyr	Val	Gln	Ser	Asn	Gly	Gly	Ala	Ile	Asn	His	
			35				40					45				

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc	192
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser	
50 55 60	
gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag	240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu	
65 70 75 80	
acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg	288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu	
85 90 95	
cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg	336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly	
100 105 110	
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc	384
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu	
115 120 125	
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac	432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp	
130 135 140	
tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc	480
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile	
145 150 155 160	
gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac	528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr	
165 170 175	
gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc	576
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly	
180 185 190	
att tcc aat tat cgt cag atc tac ccc cct aat gcc aac aag atc agg	624
Ile Ser Asn Tyr Arg Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg	
195 200 205	
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc	672
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile	
210 215 220	
aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag	720

Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln	
225	230 235 240
cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt	768
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly	
245	250 255
tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg	816
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp	
260	265 270
gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc	864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile	
275	280 285
gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg	906
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu	
290	295 300
taa	909
<210> 15	
<211> 108	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 15	
ttaagacca gtttgatctc aacgcggaga ccaacgcccg tatcaacggc aatgcccccg	60
ctgagattga tctgcgccag atgaggaccg tgactcccat ccgcatgc	108
<210> 16	
<211> 103	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 16	
cggatgggag tcacggtcct catctggcgc agatcaatct cagcgggggc attgccgttg	60
atactacggg cgttggtctc cgcgttgaga tcgaaactgg gtc	103
<210> 17	

<211> 92
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
caaggcggcc gtgggtcttg ttgggccttt tcaggcgtgg ccgcgacaga gtcggcatac 60
ctcgcgtatc ggaatcagag cctggacctc gc 92

<210> 18
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
tcagcgagggt ccaggctctg attccgatac gcgaggatatg ccgactctgt cgcggccacg 60
cctgaaaagg cccaacaaga cccacggccg ccttgcattg 99

<210> 19
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
tgagcaggag ctcgttgacc gtgcctccca acacggatgt catggggata cgattcccag 60
aggtatcgaa tacatccagc ata 83

<210> 20
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
ctggatgtat tcgatacctc tgggaatcgt atcccccatg acatccgtgt tgggaggcac 60
gggtcaacgcg ctctctgc 77

<210> 21
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 21
 actgacaggc ctcggccgag ctccattaa 29

 <210> 22
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 22
 cagtcaccta ggtctagact cgaggggat 29

 <210> 23
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 23
 ggctttcgaa caccttaaga cccag 25

 <210> 24
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 24
 gctccctagc tacgtatcgg taatagc 27

 <210> 25

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 25

cctcgcgtat cggcaacaga gcctggacc

29

<210> 26

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 26

ggtccaggct ctggttgccga tacgcgagg

29